

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 11

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 31-Mar-1997

(C) CLASSIFICATION:

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30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/625328

(B) FILING DATE: 1-Apr-1996

(vii) PRIOR APPLICATION DATA:

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(A) APPLICATION NUMBER: 08/710802

(B) FILING DATE: 23-Sep-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1007P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
1 5 10 15  
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser  
20 25 30  
Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu  
35 40 45  
Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro  
50 55 60  
Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln  
65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala  
80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu  
5 95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly  
110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro  
10 125 130 135

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His  
140 145 150

Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys  
15 155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro  
20 170 175 180

Thr  
181

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50  
 TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTCG AGAGGCTGCC 100  
 5 CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150  
 ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200  
 TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250  
 10 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300  
 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350  
 15 CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400  
 ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30 CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

- (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

10 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1438 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50  
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100  
AGCTCTATCC TGTGCCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150  
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200  
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCC GCCTCC 250  
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300  
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350  
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400

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GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450  
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500  
5 AGATTGGTCT GTTTTGTTCG AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550  
GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600  
AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCTG 650  
10 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700  
GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750  
CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800  
TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850  
GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900  
20 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950  
GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000  
CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050  
GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100  
GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACCTTCA GCCAGCATTC 1150  
30 CCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200  
GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250  
35 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300

ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350  
 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400  
 5 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 417 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
 1 5 10 15  
 20 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser  
 20 25 30  
 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu  
 35 40 45  
 25 Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro  
 50 55 60  
 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln  
 65 70 75  
 30 Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala  
 80 85 90  
 Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu  
 35 95 100 105

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	Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	
					110					115					120	
5	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro	
					125					130					135	
	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His	
					140					145					150	
10	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys	
					155					160					165	
	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	
					170					175					180	
	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	
					185					190					195	
	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	
					200					205					210	
	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	Arg	
					215					220					225	
25	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	
					230					235					240	
	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	
					245					250					255	
30	Asp	Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	
					260					265					270	
	Ile	Cys	Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	
35					275					280					285	



	Pro	Glu	Thr	Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	
					290					295					300	
5	Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr	
					305					310					315	
	Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln	
					320					325					330	
10	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala	Val	Pro	Ala	Arg	
					335					340					345	
	Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	Leu	Gly	Leu	Arg	Glu	Ala	Glu	
					350					355					360	
15	Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	Gly	Arg	Phe	Arg	Asp	Gln	Gln	
					365					370					375	
	Tyr	Glu	Met	Leu	Lys	Arg	Trp	Arg	Gln	Gln	Gln	Pro	Ala	Gly	Leu	
20					380					385					390	
	Gly	Ala	Val	Tyr	Ala	Ala	Leu	Glu	Arg	Met	Gly	Leu	Asp	Gly	Cys	
					395					400					405	
25	Val	Glu	Asp	Leu	Arg	Ser	Arg	Leu	Gln	Arg	Gly	Pro				
					410					415		417				

(2) INFORMATION FOR SEQ ID NO:7:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

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(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1634 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94

Met Glu

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CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133  
 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
                   5                                  10                                  15

5 CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172  
 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr  
                                   20                                  25

10 CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211  
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys  
                   30                                  35                                  40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGC 250  
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly  
                                   45                                  50

CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289  
 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn  
                   55                                  60                                  65

TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328  
 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
                   70                                  75                                  80

25 TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367  
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln  
                                   85                                  90

30 GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406  
 Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn  
                   95                                  100                                  105

35 TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445  
 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro  
                                   110                                  115

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GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484  
Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser  
120 125 130

5 AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523  
Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly  
135 140 145

10 GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562  
Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg  
150 155

GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601  
Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu  
160 165 170

CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640  
His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu  
175 180

GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679  
Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp  
185 190 195

25 AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718  
Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
200 205 210

30 GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757  
Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr  
215 220

35 TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796  
Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala  
225 230 235

GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835  
 Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala  
 240 245

5 ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874  
 Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu  
 250 255 260

10 GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913  
 Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln  
 265 270 275

TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952  
 Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr  
 280 285

CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991  
 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp  
 290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030  
 Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro  
 305 310

25 ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069  
 Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met  
 315 320 325

30 ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108  
 Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp  
 330 335 340

35 GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147  
 Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr  
 345 350

CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186  
Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val  
355 360 365

5 GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225  
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu  
370 375

10 AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264  
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala  
380 385 390

15 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303  
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
395 400 405

20 GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340  
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415 417

25 GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490

CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

30 TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

(2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30